Resource Summary Report

Generated by NIF on Apr 25, 2025

PASA

RRID:SCR_014656
Type: Tool

Proper Citation

PASA (RRID:SCR_014656)

Resource Information

URL: http://pasapipeline.github.io/

Proper Citation: PASA (RRID:SCR_014656)

Description: Gene structure annotation and analysis tool that uses spliced alignments of expressed transcript sequences to automatically model gene structures. It also incorporates gene structures based on transcript alignments into existing gene structure annotations. It is one component of a larger eukayotic annotation pipeline implemented at the Broad Institute.

Synonyms: Program to Assemble Spliced Alignments (PASA), Program to Assemble Spliced Alignments

Resource Type: sequence analysis software, software resource, software application, data analysis software, data processing software

Defining Citation: DOI:10.1093/nar/gkg770

Keywords: gene structure, annotation, gene structure analysis tool, spliced alignment, transcript sequence, bio.tools

Funding:

Availability: Available for download

Resource Name: PASA

Resource ID: SCR_014656

Alternate IDs: biotools:PASA

Alternate URLs: https://bio.tools/PASA

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250425T060025+0000

Ratings and Alerts

No rating or validation information has been found for PASA.

No alerts have been found for PASA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 772 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang Y, et al. (2025) Chromosome-level genome assembly of black carp Mylopharyngodon piceus using Nanopore and Hi-C technologies. Scientific data, 12(1), 145.

Yang Y, et al. (2025) Chromosome-level genome assembly of the sweet potato rot nematode Ditylenchus destructor. Scientific data, 12(1), 174.

Clancy SM, et al. (2025) The Calicophoron daubneyi genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. BMC biology, 23(1), 11.

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly Megaselia abdita: A Model Organism for Comparative Developmental Studies in Flies. bioRxiv : the preprint server for biology.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (Rosa laevigata). Scientific data, 12(1), 132.

Ma C, et al. (2025) Chromosome-level Genome Assembly and Annotation of the Arctic Moss Ptychostomum knowltonii. Genome biology and evolution, 17(1).

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest Gryllotalpa Orientalis based on genome assembly and transcriptome comparison. BMC genomics, 26(1), 33.

Krawczyk K, et al. (2025) Chromosome-scale telomere to telomere genome assembly of common crystalwort (Riccia sorocarpa Bisch.). Scientific data, 12(1), 77.

Kariba R, et al. (2025) Draft genome sequence of Kei apple, an underutilized African tree crop. Scientific data, 12(1), 70.

Ye F, et al. (2025) Comprehensive genome annotation of the model ciliate Tetrahymena thermophila by in-depth epigenetic and transcriptomic profiling. Nucleic acids research, 53(2).

Lan L, et al. (2025) Chromosome-level and haplotype-resolved genome assembly of Bougainvillea glabra. Scientific data, 12(1), 107.

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite Platynothrus peltifer. Science advances, 11(4), eadn0817.

Amiri EE, et al. (2025) Conservation of symmetry breaking at the level of chromatin accessibility between fly species with unrelated anterior determinants. bioRxiv : the preprint server for biology.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.

Medrano JF, et al. (2025) De novo whole-genome assembly and annotation of Coffea arabica var. Geisha, a high-quality coffee variety from the primary origin of coffee. G3 (Bethesda, Md.), 15(1).

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Wang GF, et al. (2025) Chromosome-level genome assembly of a destructive leaf-mining moth Eriocrania semipurpurella alpina. Scientific data, 12(1), 2.

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie Gallus gallus and Mallard Anas platyrhynchos restored the structure of chromosomes and "missing" genes in birds. Journal of animal science and biotechnology, 16(1), 9.

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. GigaScience, 14.

Li N, et al. (2025) Chromosome-scale genome assembly of three-spotted seahorse (Hippocampus trimaculatus) with a unique karyotype. Scientific data, 12(1), 49.